

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Yu, Lei
- (ii) TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arnold, White & Durkee
 - (B) STREET: P. O. Box 4433
 - (C) CITY: Houston
 - (D) STATE: TX
 - (E) COUNTRY: USA
 - (F) ZIP: 77210-4433
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Wilson, Mark B.
 - (B) REGISTRATION NUMBER: 37,259
 - (C) REFERENCE/DOCKET NUMBER: INDA005\WIM
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 512-418-3000
 - (B) TELEFAX: 512-474-7577

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (cDNA)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 214..1410
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGTGGAAGGG GGCTACAAGC AGAGGAGAAT ATCAGACGCT CAGACGTTCC CTTCTGCCTG	60
CCGCTCTTCT CTGGTTCCAC TAGGGCTGGT CCATGTAAGA ATCTGACGGA GCCTAGGGCA	120
GCTGTGAGAG GAAGAGGCTG GGGCGCGTGG AACCCGAAAA GTCTGAGTGC TCTCAGTTAC	180

AGCCTACCTA GTCCGAGCA GGCCTTCAGC ACC ATG GAC AGC AGC ACC GGC CCA	234
Met Asp Ser Ser Thr Gly Pro	
1 5	
GGG AAC ACC AGC GAC TGC TCA GAC CCC TTA GCT CAG GCA AGT TGC TCC	282
Gly Asn Thr Ser Asp Cys Ser Asp Pro Leu Ala Gln Ala Ser Cys Ser	
10 15 20	
CCA GCA CCT GGC TCC TGG CTC AAC TTG TCC CAC GTT GAT GGC AAC CAG	330
Pro Ala Pro Gly Ser Trp Leu Asn Leu Ser His Val Asp Gly Asn Gln	
25 30 35	
TCC GAT CCA TGC GGT CTG AAC CGC ACC GGG CTT GGC GGG AAC GAC AGC	378
Ser Asp Pro Cys Gly Leu Asn Arg Thr Gly Leu Gly Gly Asn Asp Ser	
40 45 50 55	
CTG TGC CCT CAG ACC GGC AGC CCT TCC ATG GTC ACA GCC ATT ACC ATC	426
Leu Cys Pro Gln Thr Gly Ser Pro Ser Met Val Thr Ala Ile Thr Ile	
60 65 70	
ATG GCC CTC TAC TCT ATC GTG TGT GTA GTG GGC CTC TTC GGA AAC TTC	474
Met Ala Leu Tyr Ser Ile Val Cys Val Val Gly Leu Phe Gly Asn Phe	
75 80 85	
CTG GTC ATG TAT GTG ATT GTA AGA TAC ACC AAA ATG AAG ACT GCC ACC	522
Leu Val Met Tyr Val Ile Val Arg Tyr Thr Lys Met Lys Thr Ala Thr	
90 95 100	
AAC ATC TAC ATT TTC AAC CTT GCT CTG GCA GAC GCC TTA GCG ACC AGT	570
Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu Ala Thr Ser	
105 110 115	
ACA CTG CCC TTT CAG AGT GTC AAC TAC CTG ATG GGA ACA TGG CCC TTC	618
Thr Leu Pro Phe Gln Ser Val Asn Tyr Leu Met Gly Thr Trp Pro Phe	
120 125 130 135	
GGA ACC ATC CTC TGC AAG ATC GTG ATC TCA ATA GAT TAC TAC AAC ATG	666
Gly Thr Ile Leu Cys Lys Ile Val Ile Ser Ile Asp Tyr Tyr Asn Met	
140 145 150	
TTC ACC AGC ATA TTC ACC CTC TGC ACC ATG AGC GTG GAC CGC TAC ATT	714
Phe Thr Ser Ile Phe Thr Leu Cys Thr Met Ser Val Asp Arg Tyr Ile	
155 160 165	
GCT GTC TGC CAC CCA GTC AAA GCC CTG GAT TTC CGT ACC CCC CGA AAT	762
Ala Val Cys His Pro Val Lys Ala Leu Asp Phe Arg Thr Pro Arg Asn	
170 175 180	
GCC AAA ATC GTC AAC GTC TGC AAC TGG ATC CTC TCT TCT GCC ATC GGT	810
Ala Lys Ile Val Asn Val Cys Asn Trp Ile Leu Ser Ser Ala Ile Gly	
185 190 195	
CTG CCT GTA ATG TTC ATG GCA ACC ACA AAA TAC AGG CAG GGG TCC ATA	858
Leu Pro Val Met Phe Met Ala Thr Thr Lys Tyr Arg Gln Gly Ser Ile	
200 205 210 215	
GAT TGC ACC CTC ACG TTC TCC CAC CCA ACC TGG TAC TGG GAG AAC CTG	906
Asp Cys Thr Leu Thr Phe Ser His Pro Thr Trp Tyr Trp Glu Asn Leu	
220 225 230	
CTC AAA ATC TGT GTC TTT ATC TTC GCT TTC ATC ATG CCG ATC CTC ATC	954
Leu Lys Ile Cys Val Phe Ile Phe Ala Phe Ile Met Pro Ile Leu Ile	
235 240 245	

ATC ACT GTG TGT TAC GGC CTG ATG ATC TTA CGA CTC AAG AGC GTT CGC Ile Thr Val Cys Tyr Gly Leu Met Ile Leu Arg Leu Lys Ser Val Arg 250 255 260	1002
ATG CTA TCG GGC TCC AAA GAA AAG GAC AGG AAT CTG CGC AGG ATC ACC Met Leu Ser Gly Ser Lys Glu Lys Asp Arg Asn Leu Arg Arg Ile Thr 265 270 275	1050
CGG ATG GTG CTG GTG GTC GTG GCT GTA TTT ATC GTC TGC TGG ACC CCC Arg Met Val Leu Val Val Val Ala Val Phe Ile Val Cys Trp Thr Pro 280 285 290 295	1098
ATC CAC ATC TAC GTC ATC ATC AAA GCG CTG ATC ACG ATT CCA GAA ACC Ile His Ile Tyr Val Ile Ile Lys Ala Leu Ile Thr Ile Pro Glu Thr 300 305 310	1146
ACA TTT CAG ACC GTT TCC TGG CAC TTC TGC ATT GCT TTG GGT TAC ACG Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile Ala Leu Gly Tyr Thr 315 320 325	1194
AAC AGC TGC CTG AAT CCA GTT CTT TAC GCC TTC CTG GAT GAA AAC TTC Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe 330 335 340	1242
AAG CGA TGC TTC AGA GAG TTC TGC ATC CCA ACC TCG TCC ACG ATC GAA Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Thr Ile Glu 345 350 355	1290
CAG CAA AAC TCC ACT CGA GTC CGT CAG AAC ACT AGG GAA CAT CCC TCC Gln Gln Asn Ser Thr Arg Val Arg Gln Asn Thr Arg Glu His Pro Ser 360 365 370 375	1338
ACG GCT AAT ACA GTG GAT CGA ACT AAC CAC CAG CTA GAA AAT CTG GAG Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Leu Glu Asn Leu Glu 380 385 390	1386
GCA GAA ACT GCT CCA TTG CCC TAACTGGGTC TCACACCATC CAGACCCTCG Ala Glu Thr Ala Pro Leu Pro 395	1437
CTAAGCTTAG AGGCCGCCAT CTACGTGGAA TCAGGTTGCT GTCAGGGTGT GTGGGAGGCT	1497
CTGGTTTCCT GAGAAACCAT CTGATCCTGC ATTCAAAGTC ATTCCTCTCT GGCTACTTCA	1557
CTCTGCACAT GAGAGATGCT CAGACTGATC AAGACCAGAA GAAAGAAGAG ACTACCGGAC	1617
A	1618

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Ser Ser Thr Gly Pro Gly Asn Thr Ser Asp Cys Ser Asp Pro 1 5 10 15
Leu Ala Gln Ala Ser Cys Ser Pro Ala Pro Gly Ser Trp Leu Asn Leu

20					25					30					
Ser	His	Val	Asp	Gly	Asn	Gln	Ser	Asp	Pro	Cys	Gly	Leu	Asn	Arg	Thr
		35					40					45			
Gly	Leu	Gly	Gly	Asn	Asp	Ser	Leu	Cys	Pro	Gln	Thr	Gly	Ser	Pro	Ser
	50					55					60				
Met	Val	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val	Cys	Val
	65					70					75				80
Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val	Arg	Tyr
				85					90					95	
Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	Ala	Leu
			100					105					110		
Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val	Asn	Tyr
		115					120					125			
Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile	Val	Ile
	130					135					140				
Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu	Cys	Thr
	145					150					155				160
Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys	Ala	Leu
				165					170					175	
Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Val	Asn	Val	Cys	Asn	Trp
			180					185					190		
Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Met	Ala	Thr	Thr
		195					200					205			
Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser	His	Pro
	210					215					220				
Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Leu	Lys	Ile	Cys	Val	Phe	Ile	Phe	Ala
	225					230					235				240
Phe	Ile	Met	Pro	Ile	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu	Met	Ile
				245					250					255	
Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu	Lys	Asp
			260					265					270		
Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val	Ala	Val
		275					280					285			
Phe	Ile	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Tyr	Val	Ile	Ile	Lys	Ala
	290					295					300				
Leu	Ile	Thr	Ile	Pro	Glu	Thr	Thr	Phe	Gln	Thr	Val	Ser	Trp	His	Phe
	305					310					315				320
Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Cys	Leu	Asn	Pro	Val	Leu	Tyr
				325					330					335	
Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Glu	Phe	Cys	Ile
			340					345				350			
Pro	Thr	Ser	Ser	Thr	Ile	Glu	Gln	Gln	Asn	Ser	Thr	Arg	Val	Arg	Gln
		355					360					365			

Asn Thr Arg Glu His Pro Ser Thr Ala Asn Thr Val Asp Arg Thr Asn
 370 375 380
 His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
 385 390 395

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1618 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 339..1235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGTGGGAAGGG GGCTACAAGC AGAGGAGAAT ATCAGACGCT CAGACGTTCC CTTCTGCCTG	60
CCGCTCTTCT CTGGTTCCAC TAGGGCTGGT CCATGTAAGA ATCTGACGGA GCCTAGGGCA	120
GCTGTGAGAG GAAGAGGCTG GGGCGCGTGG AACCCGAAAA GTCTGAGTGC TCTCAGTTAC	180
AGCCTACCTA GTCCGCAGCA GGCCTTCAGC ACCATGGACA GCAGCACCGG CCCAGGGAAC	240
ACCAGCGACT GCTCAGACCC CTTAGCTCAG GCAAGTTGCT CCCCAGCACC TGGCTCCTGG	300
CTCAACTTGT CCCACGTTGA TGGCAACCAG TCCGATCC ATG CGG TCT GAA CCG	353
Met Arg Ser Glu Pro	
1 5	
CAC CGG GCT TGG CGG GAA CGA CAG CCT GTG CCC TCA GAC CGG CAG CCC	401
His Arg Ala Trp Arg Glu Arg Gln Pro Val Pro Ser Asp Arg Gln Pro	
10 15 20	
TTC CAT GGT CAC AGC CAT TAC CAT CAT GGC CCT CTA CTC TAT CGT GTG	449
Phe His Gly His Ser His Tyr His His Gly Pro Leu Leu Tyr Arg Val	
25 30 35	
TGT AGT GGG CCT CTT CGG AAA CTT CCT GGT CAT GTA TGT GAT TGT AAG	497
Cys Ser Gly Pro Leu Arg Lys Leu Pro Gly His Val Cys Asp Cys Lys	
40 45 50	
ATA CAC CAA AAT GAA GAC TGC CAC CAA CAT CTA CAT TTT CAA CCT TGC	545
Ile His Gln Asn Glu Asp Cys His Gln His Leu His Phe Gln Pro Cys	
55 60 65	
TCT GGC AGA CGC CTT AGC GAC CAG TAC ACT GCC CTT TCA GAG TGT CAA	593
Ser Gly Arg Arg Leu Ser Asp Gln Tyr Thr Ala Leu Ser Glu Cys Gln	
70 75 80 85	
CTA CCT GAT GGG AAC ATG GCC CTT CGG AAC CAT CCT CTG CAA GAT CGT	641
Leu Pro Asp Gly Asn Met Ala Leu Arg Asn His Pro Leu Gln Asp Arg	
90 95 100	
GAT CTC AAT AGA TTA CTA CAA CAT GTT CAC CAG CAT ATT CAC CCT CTG	689
Asp Leu Asn Arg Leu Leu Gln His Val His Gln His Ile His Pro Leu	
105 110 115	

CAC CAT GAG CGT GGA CCG CTA CAT TGC TGT CTG CCA CCC AGT CAA AGC	737
His His Glu Arg Gly Pro Leu His Cys Cys Leu Pro Pro Ser Gln Ser	
120 125 130	
CCT GGA TTT CCG TAC CCC CCG AAA TGC CAA AAT CGT CAA CGT CTG CAA	785
Pro Gly Phe Pro Tyr Pro Pro Lys Cys Gln Asn Arg Gln Arg Leu Gln	
135 140 145	
CTG GAT CCT CTC TTC TGC CAT CGG TCT GCC TGT AAT GTT CAT GGC AAC	833
Leu Asp Pro Leu Phe Cys His Arg Ser Ala Cys Asn Val His Gly Asn	
150 155 160 165	
CAC AAA ATA CAG GCA GGG GTC CAT AGA TTG CAC CCT CAC GTT CTC CCA	881
His Lys Ile Gln Ala Gly Val His Arg Leu His Pro His Val Leu Pro	
170 175 180	
CCC AAC CTG GTA CTG GGA GAA CCT GCT CAA AAT CTG TGT CTT TAT CTT	929
Pro Asn Leu Val Leu Gly Glu Pro Ala Gln Asn Leu Cys Leu Tyr Leu	
185 190 195	
CGC TTT CAT CAT GCC GAT CCT CAT CAT CAC TGT GTG TTA CGG CCT GAT	977
Arg Phe His His Ala Asp Pro His His His Cys Val Leu Arg Pro Asp	
200 205 210	
GAT CTT ACG ACT CAA GAG CGT TCG CAT GCT ATC GGG CTC CAA AGA AAA	1025
Asp Leu Thr Thr Gln Glu Arg Ser His Ala Ile Gly Leu Gln Arg Lys	
215 220 225	
GGA CAG GAA TCT GCG CAG GAT CAC CCG GAT GGT GCT GGT GGT CGT GGC	1073
Gly Gln Glu Ser Ala Gln Asp His Pro Asp Gly Ala Gly Gly Arg Gly	
230 235 240 245	
TGT ATT TAT CGT CTG CTG GAC CCC CAT CCA CAT CTA CGT CAT CAT CAA	1121
Cys Ile Tyr Arg Leu Leu Asp Pro His Pro His Leu Arg His His Gln	
250 255 260	
AGC GCT GAT CAC GAT TCC AGA AAC CAC ATT TCA GAC CGT TTC CTG GCA	1169
Ser Ala Asp His Asp Ser Arg Asn His Ile Ser Asp Arg Phe Leu Ala	
265 270 275	
CTT CTG CAT TGC TTT GGG TTA CAC GAA CAG CTG CCT GAA TCC AGT TCT	1217
Leu Leu His Cys Phe Gly Leu His Glu Gln Leu Pro Glu Ser Ser Ser	
280 285 290	
TTA CGC CTT CCT GGA TGAAACTTC AAGCGATGCT TCAGAGAGTT CTGCATCCCA	1272
Leu Arg Leu Pro Gly	
295	
ACCTCGTCCA CGATCGAACA GCAAACTCC ACTCGAGTCC GTCAGAACAC TAGGGAACAT	1332
CCCTCCACGG CTAATACAGT GGATCGAACT AACCACCAGC TAGAAAATCT GGAGGCAGAA	1392
ACTGCTCCAT TGCCCTAACT GGGTCTCACA CCATCCAGAC CCTCGCTAAG CTTAGAGGCC	1452
GCCATCTACG TGGAATCAGG TTGCTGTCAG GGTGTGTGGG AGGCTCTGGT TTCCTGAGAA	1512
ACCATCTGAT CCTGCATTCA AAGTCATTCC TCTCTGGCTA CTTCACTCTG CACATGAGAG	1572
ATGCTCAGAC TGATCAAGAC CAGAAGAAAG AAGAGACTAC CGGACA	1618

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

~~179~~
178

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

~~180~~
179

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATCTTCACCC TCACCATGAT G

21

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGTCCTTCT CCTTGAACC

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGATGAGCC TCTGTGAACT ACTAAGGTGG GAGGGGGCTA TACGCAGAGG AGAATGTCAG	60
ATGCTCAGCT CGGTCCCCTC CGCCTGACGC TCCTCTCTGT CTCAGCCAGG ACTGGTTTCT	120
GTAAGAAACA GCAGGAGCTG TGGCAGCGGC GAAAGGAAGC GGCTGAGGCG CTTGGAACCC	180
GAAAAGTCTC GGTGCTCCTG GCTACCTCGC ACAGCGTGCC CGCCCGGCCG TCAGTACCAT	240
GGACAGCAGC GCTGCCCCCA CGAACGCCAG CAATTGCACT GATGCCTTGG CGTACTCAAG	300
TTGCTCCCCA GCACCCAGCC CCGGTTCTTG GGTCAACTTG TCCCACTTAG ATGGCAACCT	360
GTCCGACCCA TGCGGTCCGA ACCGCACCGA CCTGGGCGGG AGAGACAGCC TGTGCCCTCC	420
GACCGGCAGT CCCTCCATGA TCACGGCCAT CACGATCATG GCCCTCTACT CCATCGTGTG	480
CGTGGTGGGG CTCTTCGGAA ACTTCCTGGT CATGTATGTG ATTGTCAGAT ACACCAAGAT	540
GAAGACTGCC ACCAACATCT ACATTTTCAA CCTTGCTCTG GCAGATGCCT TAGCCACCAG	600
TACCCTGCCC TTCCAGAGTG TGAATTACCT AATGGGAACA TGGCCATTG GAACCATCCT	660

181
180

TTGCAAGATA GTGATCTCCA TAGATTACTA TAACATGTTC ACCAGCATAT TCACCCTCTG 720
 CACCATGAGT GTTGATCGAT ACATTGCAGT CTGCCACCCCT GTCAAGGCCT TAGATTTCCG 780
 TACTCCCCGA AATGCCAAAA TTATCAATGT CTGCAACTGG ATCCTCTCTT CAGCCATTGG 840
 TCTTCCTGTA ATGTTTCATGG CTACAACAAA ATACAGGCAA GGTTCATAG ATTGTACACT 900
 AACATTCTCT CATCCAACCT GGTACTGGGA AAACCTGCTG AAGATCTGTG TTTTCATCTT 960
 CGCCTTCATT ATGCCAGTGC TCATCATTAC CGTGTGCTAT GGAAGTATGA TCTTGCGCCT 1020
 CAAGAGTGTC CGCATGCTCT CTGGCTCCAA AGAAAAGGAC AGGAATCTTC GAAGGATCAC 1080
 CAGGATGGTG CTGGTGGTGG TGGCTGTGTT CATCGTCTGC TGGACTCCCA TTCACATTTA 1140
 CGTCATCATT AAAGCCTTGG TTACAATCCC AGAAACTACG TTCCAGACTG TTTCTTGGCA 1200
 CTTCTGCATT GCTCTAGGTT ACACAAACAG CTGCCTCAAC CCAGTCCTTT ATGCATTTCT 1260
 GGATGAAAAC TTCAAACGAT GCTTCAGAGA GTTCTGTATC CCAACCTCTT CCAACATTGA 1320
 GCAACAAAAC TCCACTCGAA TTCGTCAGAA CACTAGAGAC CACCCCTCCA CGGCCAATAC 1380
 AGTGGATAGA ACTAATCATC AGCTAGAAAA TCTGGAAGCA GAAACTGCTC CGTTGCCCTA 1440
 ACAGGGTCTC ATGCCATTCC GACCTTCACC AAGCTTAGAA GCCACCATGT ATGTGGAAGC 1500
 AGGTTGCTTC AAGAATGTGT AGGAGGCTCT AATTCTCTAG GAAAGTGCCT GCTTTTAGGT 1560
 CATCCAACCT CTTTCCTCTC TGGCCACTCT GCTCTGCACA TTAGAGGCCG 1610

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
 1 5 10 15
 Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
 20 25 30
 Asn Leu Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn
 35 40 45
 Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
 50 55 60
 Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
 65 70 75 80
 Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
 85 90 95
 Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
 100 105 110

Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
115 120 125

Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
130 135 140

Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
145 150 155 160

Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
165 170 175

Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
180 185 190

Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
195 200 205

Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
210 215 220

His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile
225 230 235 240

Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
245 250 255

Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
260 265 270

Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
275 280 285

Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
290 295 300

Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
305 310 315 320

His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
325 330 335

Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
340 345 350

Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
355 360 365

Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
370 375 380

Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
385 390 395 400

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGAAGACTGC CACCAACA

18

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATGACGTAG ATGTGGAT

18

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTCGGATCCG TATTATGTCT G

21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATAGTCGACT AAAACTAAAT C

21

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACYGCMACCA ACATCTACAT

20

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCTRGTRAAC ATGTTGTAGT A

21

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 173..1273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCATTCCCAG CCGCAGCAGA CCCCAATCTA GAGTGAGAGT CATTGCTCAG TCCACTGTGC	60
TCCTGCCTGC CCGCCTTTCT GCTAAGCATT GGGGTCTATT TTGGCCCAGC TTCTGAAGAG	120
GCTGTGTGTG CCGTTGGAGG AACTGTACTG AGTGGCTTTG CAGGGTGACA GC ATG	175
	Met
	1
GAG TCC CTC TTT CCT GCT CCA TAC TGG GAG GTC TTG TAT GGC AGC CAC	223
Glu Ser Leu Phe Pro Ala Pro Tyr Trp Glu Val Leu Tyr Gly Ser His	
5 10 15	
TTT CAA GGG AAC CTG TCC CTC CTA AAT GAG ACC GTA CCC CAC CAC CTG	271
Phe Gln Gly Asn Leu Ser Leu Leu Asn Glu Thr Val Pro His His Leu	
20 25 30	
CTC CTC AAT GCT AGT CAC AGC GCC TTC CTG CCC CTT GGA CTC AAG GTC	319
Leu Leu Asn Ala Ser His Ser Ala Phe Leu Pro Leu Gly Leu Lys Val	

185
184

35	40	45	
ACC ATC GTG GGG CTC TAC TTG GCT GTG TGC ATC GGG GGG CTC CTG GGG Thr Ile Val Gly Leu Tyr Leu Ala Val Cys Ile Gly Gly Leu Leu Gly 50 55 60 65			367
AAC TGC CTC GTC ATG TAT GTC ATC CTC AGG CAC ACC AAG ATG AAG ACA Asn Cys Leu Val Met Tyr Val Ile Leu Arg His Thr Lys Met Lys Thr 70 75 80			415
GCT ACC AAC ATT TAC ATA TTT AAT CTG GCA CTG GCT GAT ACC CTG GTC Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Thr Leu Val 85 90 95			463
TTG CTA ACA CTG CCC TTC CAG GGC ACA GAC ATC CTA CTG GGC TTC TGG Leu Leu Thr Leu Pro Phe Gln Gly Thr Asp Ile Leu Leu Gly Phe Trp 100 105 110			511
CCA TTT GGG AAT GCA CTC TGC AAG ACT GTC ATT GCT ATC GAC TAC TAC Pro Phe Gly Asn Ala Leu Cys Lys Thr Val Ile Ala Ile Asp Tyr Tyr 115 120 125			559
AAC ATG TTT ACC AGC ACT TTT ACT CTG ACC GCC ATG AGC GTA GAC CGC Asn Met Phe Thr Ser Thr Phe Thr Leu Thr Ala Met Ser Val Asp Arg 130 135 140 145			607
TAT GTG GCT ATC TGC CAC CCT ATC CGT GCC CTT GAT GTT CGG ACA TCC Tyr Val Ala Ile Cys His Pro Ile Arg Ala Leu Asp Val Arg Thr Ser 150 155 160			655
AGC AAA GCC CAG GCT GTT AAT GTG GCC ATA TGG GCC CTG GCT TCA GTG Ser Lys Ala Gln Ala Val Asn Val Ala Ile Trp Ala Leu Ala Ser Val 165 170 175			703
GTT GGT GTT CCT GTT GCC ATC ATG GGT TCA GCA CAA GTG GAA GAT GAA Val Gly Val Pro Val Ala Ile Met Gly Ser Ala Gln Val Glu Asp Glu 180 185 190			751
GAG ATC GAG TGC CTG GTG GAG ATC CCT GCC CCT CAG GAC TAT TGG GGC Glu Ile Glu Cys Leu Val Glu Ile Pro Ala Pro Gln Asp Tyr Trp Gly 195 200 205			799
CCT GTA TTC GCC ATC TGC ATC TTC CTT TTT TCC TTC ATC ATC CCT GTG Pro Val Phe Ala Ile Cys Ile Phe Leu Phe Ser Phe Ile Ile Pro Val 210 215 220 225			847
CTG ATC ATC TCT GTC TGC TAC AGC CTC ATG ATT CGA CGA CTT CGT GGT Leu Ile Ile Ser Val Cys Tyr Ser Leu Met Ile Arg Arg Leu Arg Gly 230 235 240			895
GTC CGT CTG CTT TCA GGC TCC CGG GAG AAG GAC CGA AAC CTG CGG CGT Val Arg Leu Leu Ser Gly Ser Arg Glu Lys Asp Arg Asn Leu Arg Arg 245 250 255			943
ATC ACT CGA CTG GTG CTG GTA GTG GTG GCT GTG TTT GTG GGC TGC TGG Ile Thr Arg Leu Val Leu Val Val Val Ala Val Phe Val Gly Cys Trp 260 265 270			991
ACG CCT GTG CAG GTG TTT GTC CTG GTT CAA GGA CTG GGT GTT CAG CCA Thr Pro Val Gln Val Phe Val Leu Val Gln Gly Leu Gly Val Gln Pro 275 280 285			1039
GGT AGT GAG ACT GCA GTT GCC ATC CTG CGC TTC TGC ACA GCC CTG GGC Gly Ser Glu Thr Ala Val Ala Ile Leu Arg Phe Cys Thr Ala Leu Gly 285 290 295			1087

290	295	300	305	
TAT GTC AAC AGT TGT CTC AAT CCC ATT CTC TAT GCT TTC CTG GAT GAG				1135
Tyr Val Asn Ser Cys Leu Asn Pro Ile Leu Tyr Ala Phe Leu Asp Glu	310	315	320	
AAC TTC AAG GCC TGC TTT AGA AAG TTC TGC TGT GCT TCA TCC CTG CAC				1183
Asn Phe Lys Ala Cys Phe Arg Lys Phe Cys Cys Ala Ser Ser Leu His	325	330	335	
CGG GAG ATG CAG GTT TCT GAT CGT GTG CGG AGC ATT GCC AAG GAT GTT				1231
Arg Glu Met Gln Val Ser Asp Arg Val Arg Ser Ile Ala Lys Asp Val	340	345	350	
GGC CTT GGT TGC AAG ACT TCT GAG ACA GTA CCA CGG CCA GCA				1273
Gly Leu Gly Cys Lys Thr Ser Glu Thr Val Pro Arg Pro Ala	355	360	365	
TGACTAGGCG TGGACCTGCC CATGGTGCCT GTCAGCCCAC AGAGCCCATC TACACCCAAC				1333
ACGGAGCTCA CACAGGTCAC TGCTCTCTAG GTTGACCCTG AACCTTGAGC ATCTGGAGCC				1393
TTGAATGGCT TTTCTTTTGG ATCAGGATGC TCAGTCCTAG AGGAAGACCT TTTAGCACCA				1453
TGGGACAGGT CAAAGCATCA AGGTGGTCTC CATGGCCTCT GTCAGATTAA GTTCCCTCCC				1513
TGGTATAGGA CCAGAGAGGA CCAAAGGAAC TGAATAGAAA CATCCACAAC ACAG				1567

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Glu	Ser	Leu	Phe	Pro	Ala	Pro	Tyr	Trp	Glu	Val	Leu	Tyr	Gly	Ser
1				5					10					15	
His	Phe	Gln	Gly	Asn	Leu	Ser	Leu	Leu	Asn	Glu	Thr	Val	Pro	His	His
		20						25					30		
Leu	Leu	Leu	Asn	Ala	Ser	His	Ser	Ala	Phe	Leu	Pro	Leu	Gly	Leu	Lys
		35					40					45			
Val	Thr	Ile	Val	Gly	Leu	Tyr	Leu	Ala	Val	Cys	Ile	Gly	Gly	Leu	Leu
	50				55					60					
Gly	Asn	Cys	Leu	Val	Met	Tyr	Val	Ile	Leu	Arg	His	Thr	Lys	Met	Lys
65					70				75					80	
Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Thr	Leu
			85					90						95	
Val	Leu	Leu	Thr	Leu	Pro	Phe	Gln	Gly	Thr	Asp	Ile	Leu	Leu	Gly	Phe
			100					105					110		
Trp	Pro	Phe	Gly	Asn	Ala	Leu	Cys	Lys	Thr	Val	Ile	Ala	Ile	Asp	Tyr
		115					120					125			

Tyr	Asn	Met	Phe	Thr	Ser	Thr	Phe	Thr	Leu	Thr	Ala	Met	Ser	Val	Asp
130						135					140				
Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Ile	Arg	Ala	Leu	Asp	Val	Arg	Thr
145					150					155					160
Ser	Ser	Lys	Ala	Gln	Ala	Val	Asn	Val	Ala	Ile	Trp	Ala	Leu	Ala	Ser
				165					170					175	
Val	Val	Gly	Val	Pro	Val	Ala	Ile	Met	Gly	Ser	Ala	Gln	Val	Glu	Asp
			180					185					190		
Glu	Glu	Ile	Glu	Cys	Leu	Val	Glu	Ile	Pro	Ala	Pro	Gln	Asp	Tyr	Trp
		195					200					205			
Gly	Pro	Val	Phe	Ala	Ile	Cys	Ile	Phe	Leu	Phe	Ser	Phe	Ile	Ile	Pro
	210					215					220				
Val	Leu	Ile	Ile	Ser	Val	Cys	Tyr	Ser	Leu	Met	Ile	Arg	Arg	Leu	Arg
225					230					235					240
Gly	Val	Arg	Leu	Leu	Ser	Gly	Ser	Arg	Glu	Lys	Asp	Arg	Asn	Leu	Arg
				245					250					255	
Arg	Ile	Thr	Arg	Leu	Val	Leu	Val	Val	Val	Ala	Val	Phe	Val	Gly	Cys
			260					265					270		
Trp	Thr	Pro	Val	Gln	Val	Phe	Val	Leu	Val	Gln	Gly	Leu	Gly	Val	Gln
		275					280					285			
Pro	Gly	Ser	Glu	Thr	Ala	Val	Ala	Ile	Leu	Arg	Phe	Cys	Thr	Ala	Leu
	290					295					300				
Gly	Tyr	Val	Asn	Ser	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	Ala	Phe	Leu	Asp
305					310					315					320
Glu	Asn	Phe	Lys	Ala	Cys	Phe	Arg	Lys	Phe	Cys	Cys	Ala	Ser	Ser	Leu
				325					330					335	
His	Arg	Glu	Met	Gln	Val	Ser	Asp	Arg	Val	Arg	Ser	Ile	Ala	Lys	Asp
			340					345					350		
Val	Gly	Leu	Gly	Cys	Lys	Thr	Ser	Glu	Thr	Val	Pro	Arg	Pro	Ala	
		355					360					365			